P0573: Comparative Transcriptomics Among Wild and Modern Cotton

POSTER

Gossypium hirsutum is the main cotton cultivated species because of its agronomically and fiber qualities. These traits had undergone different processes of selection and genetic improvement. In order to contribute to the study of cotton domestication we present global transcriptome analyses of wild and modern cotton using RNA-seq. Approximately 2000 genes were differentially expressed between wild and domesticated accessions. We also found a different expression contribution of homeologous genes, contained in each cotton subgenomes (A/D). Functional enrichment analysis showed that cellular component morphogenesis and cell wall organization genes were significantly represented in domesticated than wild cotton. Several other transcripts differences may provide clues about genes and processes that have been selected during domestication and breeding of modern lines.

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